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              RAW SEQUENCE LISTING            DATE: 02/12/2001
              PATENT APPLICATION:  US/09/242,657B    TIME: 10:52:56

              Input Set : A:\Pto.amc
              Output Set: N:\CRF3\02122001\I242657B.raw

              SEQUENCE LISTING
   3 (1) GENERAL INFORMATION:
   4      (i) APPLICANT: Peter Ruhdal Jensen
   5                      Karin Hammer
   7     (ii) TITLE OF INVENTION: Artificial promoter libraries
   8                              for selected organisms and promoters derived from such
   9                              libraries
  11    (iii) NUMBER OF SEQUENCES: 58
  13     (iv) CORRESPONDENCE ADDRESS:
  14          (A) ADDRESSEE: Stanislaus Aksman
  15                          Hunton & Williams
  16          (B) STREET: 1900 K Street, NW
  17          (C) CITY: Washington, DC
  18          (E) COUNTRY: USA
  19          (F) ZIP: 20006-1109
  21      (v) COMPUTER READABLE FORM:
  22          (A) MEDIUM TYPE: Floppy disk
  23          (B) COMPUTER: IBM PC compatible
  24          (C) OPERATING SYSTEM: PC-DOS/MS-DOS
  25          (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
  26                        (EPO)
  28     (vi) CURRENT APPLICATION DATA:
C--> 29         (A) APPLICATION NUMBER: US/09/242,657B
C--> 30         (B) FILING DATE: 19-Feb-1999
  32    (vii) PRIOR APPLICATION DATA:
  33          (A) APPLICATION NUMBER: DK 886/96
  34          (B) FILING DATE: 23-AUG-1996
  35          (A) APPLICATION NUMBER: PCT/DK97/00342
  36          (B) FILING DATE: August 25, 1997
  38   (viii) ATTORNEY/AGENT INFORMATION:
C--> 39         (C) REFERENCE/DOCKET NUMBER: 55411.000002
  41     (ix) TELECOMMUNICATION INFORMATION:
  42          (A) TELEPHONE: (202) 955-1500
  43          (B) TELEFAX: (202) 778-2201
  45 (2) INFORMATION FOR SEQ ID NO: 1:
  47      (i) SEQUENCE CHARACTERISTICS:
  48          (A) LENGTH: 100 base pairs
  49          (B) TYPE: nucleic acid
  50          (C) STRANDEDNESS: double
  51          (D) TOPOLOGY: linear
  53     (ii) MOLECULE TYPE: DNA (genomic)
  55    (iii) HYPOTHETICAL: YES
  56     (iv) ANTI-SENSE: NO
  58     (vi) ORIGINAL SOURCE:
  59          (A) ORGANISM: Lactococcus lactis
  61     (ix) FEATURE:
  62          (A) NAME/KEY: promoter
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63   (B) LOCATION:26..82
64   (C) IDENTIFICATION METHOD: experimental
65   (D) OTHER INFORMATION:/evidence= EXPERIMENTAL
66 /standard_name= "Artificial promoter library" /note= "A
67 degenerated sequence specifying a mixture of artificial
68 promoters covering a wide range of expression in small steps
69 in L. lactis"
71   (ix) FEATURE:
72   (A) NAME/KEY: misc_feature
73   (B) LOCATION:31..45
74   (D) OTHER INFORMATION:/standard_name= "Consensus
75 sequence"
77   (ix) FEATURE:
78   (A) NAME/KEY: misc_feature
79   (B) LOCATION:60..69
80   (D) OTHER INFORMATION:/standard_name= "Consensus
81 sequence"
83   (ix) FEATURE:
84   (A) NAME/KEY: misc_feature
85 ·   (B) LOCATION:74..82
86   (D) OTHER INFORMATION:/standard_name= "Consensus
87 sequence"
89   (ix) FEATURE:
90   (A) NAME/KEY: -35_signal
91   (B) LOCATION:40..45
92   (D) OTHER INFORMATION:/standard_name= "-35 box"
94   (ix) FEATURE:
95   (A) NAME/KEY: -10_signal
96   (B) LOCATION:63..68
97   (D) OTHER INFORMATION:/standard_name= "Pribnow box"
99   (ix) FEATURE:
100   (A) NAME/KEY: misc_recomb
101   (B) LOCATION:3..25
102   (C) IDENTIFICATION METHOD: experimental
103   (D) OTHER INFORMATION:/evidence= EXPERIMENTAL
104 /standard_name= "Multiple cloning site" /label= MCS
105 /note= "A sequence specifying recognition sites
106 for the restriction endonucleases: NlaIV, BstYI, BamHI, AlwI,
107 MboI,
108 DpnI, AflII, MseI, SspI, NsiI."
110   (ix) FEATURE:
111   (A) NAME/KEY: misc_recomb
112   (B) LOCATION:74..98
113   (C) IDENTIFICATION METHOD: experimental
114   (D) OTHER INFORMATION:/evidence= EXPERIMENTAL
115 /standard_name= "Multiple cloning site"
116 /label= MCS
117 /note= "A sequence specifying recognition sites
118 for the restriction endonucleases: ScaI, RsaI, HpaI, HincII,

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119 MseI, SfcI,
120 PstI, Fnu4HI, BbvI, PvuII, NspBII, AluI, EcoRI."
122   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
124 CGGGATCCTT AAGAATATTA TGCATNNNNN AGTTTATTCT TGACANNNNN NNNNNNNNNT 60
126 GGTATAATAN NANAGTACTG TTAACTGCAG CTGAATTCGG   100
128 (2) INFORMATION FOR SEQ ID NO: 2:
130   (i) SEQUENCE CHARACTERISTICS:
131   (A) LENGTH: 113 base pairs
132   (B) TYPE: nucleic acid
133   (C) STRANDEDNESS: double
134   (D) TOPOLOGY: linear
136   (ii) MOLECULE TYPE: DNA (genomic)
138   (iii) HYPOTHETICAL: YES
140   (iv) ANTI-SENSE: NO
142   (ix) FEATURE:
143   (A) NAME/KEY: promoter
144   (B) LOCATION:23..95
145   (D) OTHER INFORMATION:/standard_name=
146 "Artificial promoter library"
147 /note= "A degenerated sequence specifying a mixture
148 of artificial temperature regulated promoters covering a wide
149 range of expression in small steps in L. lactis"
151   (ix) FEATURE:
152   (A) NAME/KEY: misc_feature
153   (B) LOCATION:23..49
154   (D) OTHER INFORMATION:/standard_name=
155 "Sequence providing temperature regulation to promoters"
156 /note= "This sequence comprising two inverted
157 repeats separated by a short spacer provides temperature (heat
158 shock) regulation to promoters in Gram-positive bacteria"
160   (ix) FEATURE:
161   (A) NAME/KEY: misc_feature
162   (B) LOCATION:50..60
163   (D) OTHER INFORMATION:/standard_name=
164 "Consensus sequence"
166   (ix) FEATURE:
167   (A) NAME/KEY: misc_feature
168   (B) LOCATION:75..84
169   (D) OTHER INFORMATION:/standard_name= "Consensus
170 sequence"
172   (ix) FEATURE:
173   (A) NAME/KEY: misc_feature
174   (B) LOCATION:89..95
175   (D) OTHER INFORMATION:/standard_name= "Consensus
176 sequence"
178   (ix) FEATURE:
179   (A) NAME/KEY: -35_signal
180   (B) LOCATION:55..60
181   (D) OTHER INFORMATION:/standard_name= "-35 box"

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183      (ix) FEATURE:
184            (A) NAME/KEY: -10_signal
185            (B) LOCATION:78..83
186            (D) OTHER INFORMATION:/standard_name= "Pribnow box"
188      (ix) FEATURE:
189            (A) NAME/KEY: misc_recomb
190            (B) LOCATION:3..22
191            (D) OTHER INFORMATION:/standard_name= "Multiple
192 cloning site"
193 /label= MCS
194 /note= "A sequence specifying recognition sites
195 for the restriction endonucleases: NlaIV, BstYI, BamHI, AlwI,
196 MboI,DpnI, HindIII, AluI, MseI (2 sites), SspI, AseI."
198      (ix) FEATURE:
199            (A) NAME/KEY: misc_recomb
200            (B) LOCATION:89..111
201            (D) OTHER INFORMATION:/standard_name= "Multiple
202 cloning site"
203 /label= MCS
204 /note= "A sequence specifying recognition sites
205 for the restriction endonucleases: ScaI, RsaI, SfcI, PstI,
206 Fnu4HI, BbvI,
207 PvuII, NspBII, AluI, XbaI, MaeI, EcoRI, ApoI."
209      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
211 CGGGATCCAA GCTTAATATT AATTAGCACT CNNNNNNNNN GAGTGCTAAT TTTTTTGACA 60
213 NNNNNNNNNN NNNNTGGTAT AATANNANAG TACTGCAGCT GTCTAGAATT CGG       113
215 (2) INFORMATION FOR SEQ ID NO: 3:
217      (i) SEQUENCE CHARACTERISTICS:
218            (A) LENGTH: 199 base pairs
219            (B) TYPE: nucleic acid
220            (C) STRANDEDNESS: double
221            (D) TOPOLOGY: linear
223      (ii) MOLECULE TYPE: DNA (genomic)
225      (iii) HYPOTHETICAL: YES
227      (iv) ANTI-SENSE: NO
229      (vi) ORIGINAL SOURCE:
230            (A) ORGANISM: Saccharomyces cerevisiae
232      (ix) FEATURE:
233            (A) NAME/KEY: protein_bind
234            (B) LOCATION:10..16
235            (D) OTHER INFORMATION:/function= "Activating
236 promoters in
237 S. cerevisiae"
238 /bound_moiety= "GCN4 protein"
239 /standard_name= "Upstream activating sequence" /label=
240 UAS_GCN4p
241 /note= "A DNA sequence that specifies a binding
242 site for the GCN4 protein, which activates the transcription
243 of genes involved in amino acid synthesis in S. cerevisiae."
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                    Input Set : A:\Pto.amc
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245      (ix) FEATURE:
246              (A) NAME/KEY: TATA_signal
247              (B) LOCATION:67..72
248              (D) OTHER INFORMATION:/standard_name= "TATA box"
250      (ix) FEATURE:
251              (A) NAME/KEY: misc_signal
252              (B) LOCATION:122..144
253              (D) OTHER INFORMATION:/function= "Transcription
254 initiation"
255 /standard_name= "TI box"
257      (ix) FEATURE:
258              (A) NAME/KEY: protein_bind
259              (B) LOCATION:122..144
260              (D) OTHER INFORMATION:/bound_moiety= "Arginine
261 repressor"
262 /standard_name= "arginine repressor binding
263 site"
264 /label= argR
266      (ix) FEATURE:
267              (A) NAME/KEY: misc_RNA
268              (B) LOCATION:145..192
269              (D) OTHER INFORMATION:/function= "Spacer"
270 /standard_name= "Part of native sequence for
271 ARG8
272 gene incl. first codon"
274      (ix) FEATURE:
275              (A) NAME/KEY: misc_recomb
276              (B) LOCATION:3..8
277              (D) OTHER INFORMATION:/standard_name= "Recognition
278 site for restriction endonuclease EcoRI"
279 /label= EcoRI_site
281      (ix) FEATURE:
282              (A) NAME/KEY: misc_recomb
283              (B) LOCATION:192..197
284              (D) OTHER INFORMATION:/standard_name= "Recognition
285 site or restriction endonuclease BamHI"
286 /label= BamHI_site
288      (ix) FEATURE:
289              (A) NAME/KEY: promoter
290              (B) LOCATION:10..192
291              (D) OTHER INFORMATION:/standard_name= "Artificial
292 promoter library"
293 /note= "A degenerated sequence specifying a mixture
294 of
295 artificial promoters covering a wide range of
296 expression in small steps in S. cerevisiae"
298      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
300 CAGAATTCGT GACTCANNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN 60
302 NNNNNNNNNN NNNNNNTATA AANNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN 120
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VERIFICATION SUMMARY   DATE: 02/12/2001
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L:29 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:30 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:39 M:220 C: Keyword misspelled or invalid format, [(C) REFERENCE/DOCKET NUMBER:]